What is claimed:

1. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID Nos 1 to 4, 6 and 31, or the complements thereof, wherein said contiguous span comprises:

- at least one of the following nucleotide positions of SEQ ID No 1: 1 to 3585 and 4644 to 5222; and/or
- at least one of the following nucleotide positions of SEQ ID No 2: 1 to 16155 and 16331 to 21278; and/or
- at least one of the following nucleotide positions of SEQ ID No 3: 1 to 5531 and 6355 to 21636; and/or
- at least one of the following nucleotide positions of SEQ ID No 4: 1 to 519 and 2563 to 5566; and/or
- at least one of the following nucleotide positions of SEQ ID No 6: 1 to 1791.

2. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No 31, or the complements thereof, wherein said contiguous span comprises at least one of the following nucleotide positions of SEQ ID No 31: 1 to 480 and 717 to 983.

3. An isolated, purified, or recombinant polynucleotide consisting essentially of a contiguous span of 8 to 50 nucleotides of anyone of SEQ ID Nos 1 to 3 and 32 to 69 or the complement thereof, wherein said span includes a *G713 or 13q31-q33*-related biallelic marker in said sequence.

4. A polynucleotide according to claim 3, wherein said *G713 or 13q31-q33*-related biallelic marker is selected from the group consisting of A1 to A49, and the complements thereof.

5. A polynucleotide according to claim 3, wherein said *13q31-q33*-related biallelic marker is selected from the group consisting of A16 to A20 and the complements thereof.

6. A polynucleotide according to claim 3, wherein said contiguous span is 18 to 35 nucleotides in length and said biallelic marker is within 4 nucleotides of the center of said polynucleotide.

7. A polynucleotide according to claim 6, wherein said polynucleotide consists of said contiguous span and said contiguous span is 25 nucleotides in length and said biallelic marker is at the center of said polynucleotide.

8. A polynucleotide according to claim 6, wherein said polynucleotide consists essentially of a sequence selected from the following sequences: P1 to P49, and the complementary sequences thereto.

9. A polynucleotide according to any one of claims 1, 2 or 3, wherein the 3' end of said contiguous span is present at the 3' end of said polynucleotide.

10. A polynucleotide according to claim 3, wherein the 3' end of said contiguous span is located at the 3' end of said polynucleotide and said biallelic marker is present at the 3' end of said polynucleotide.

11. An isolated, purified, or recombinant polynucleotide consisting essentially of a contiguous span of 8 to 50 nucleotides of anyone of SEQ ID Nos 1 to 3 and 32 to 69 or the complement thereof, wherein the 3' end of said contiguous span is located at the 3' end of said polynucleotide, and wherein the 3' end of said polynucleotide is located within 20 nucleotides upstream of a *G713 or 13q31-q33*-related biallelic marker in said sequence.

12. A polynucleotide according to claim 11, wherein the 3' end of said polynucleotide is located 1 nucleotide upstream of said *G713 or 13q31-q33*-related biallelic marker in said sequence.

13. A polynucleotide according to claim 12, wherein said polynucleotide consists essentially of a sequence selected from the following sequences: D1 to D49, and E1 to E49.

14. An isolated, purified, or recombinant polynucleotide consisting essentially of a sequence selected from the following sequences: B1 to B49 and C1 to C49.

15. An isolated, purified, or recombinant polynucleotide which encodes a polypeptide comprising a contiguous span of at least 6 amino acids of SEQ ID Nos 5 or 7.

16. A polynucleotide for use in a genotyping assay for determining the identity of the nucleotide at a *G713- or 13q31-q33*-related biallelic marker, or the complement thereof.

17. A polynucleotide according to claim 16, wherein the polynucleotide is used in an assay selected from the group consisting of a hybridization assay, a sequencing assay, a microsequencing assay and a mismatch detection assay.

18. A polynucleotide according to claim 16, wherein the polynucleotide is used in amplifying a segment of nucleotides comprising said biallelic marker.

19. A polynucleotide according to any one of claims 1, 2, 3, 11 and 14 to 16 attached to a solid support.

20. An array of polynucleotides comprising at least one polynucleotide according to claim 19.

21. An array according to claim 20, wherein said array is addressable.

22. A polynucleotide according to any one of claims 1, 2, 3, 11 and 14 to 16 further comprising a label.

23. A recombinant vector comprising a polynucleotide according to any one of claims 1, 2, or 15.

24. A host cell comprising a recombinant vector according to claim 23.

25. A non-human host animal or mammal comprising a recombinant vector according to claim 23.

26. A mammalian host cell comprising a *G713* gene disrupted by homologous recombination with a knock out vector, comprising a polynucleotide according to any one of claims 1, 2, or 15.

27. A non-human host mammal comprising a *G713* gene disrupted by homologous recombination with a knock out vector, comprising a polynucleotide according to any one of claims 1, 2, or 15.

28. A method of genotyping comprising determining the identity of a nucleotide at a *G713- or 13q31-q33*-related biallelic marker or the complement thereof in a biological sample.

29. A method according to claim 28, wherein said biological sample is derived from a single subject.

30. A method according to claim 29, wherein the identity of the nucleotides at said biallelic marker is determined for both copies of said biallelic marker present in said individual's genome.

31. A method according to claim 28, wherein said biological sample is derived from multiple subjects.

32. A method according to claim 28, further comprising amplifying a portion of said sequence comprising the biallelic marker prior to said determining step.

33. A method according to claim 32, wherein said amplifying is performed by PCR.

34. A method according to claim 28, wherein said determining is performed by an an assay selected from the group consisting of a hybridization assay, a sequencing assay, a microsequencing assay and an enzyme-based mismatch assay.

35. A method of estimating the frequency of an allele of a *G713- or 13q31-q33*-related biallelic marker in a population comprising:

a) genotyping individuals from said population for said biallelic marker according to the method of claim 28; and

b) determining the proportional representation of said biallelic marker in said population.

36. A method of detecting an association between a genotype and a trait, comprising the steps of:
a) determining the frequency of at least one *G713- or 13q31-q33*-related biallelic marker in trait positive population according to the method of claim 35;
b) determining the frequency of at least one *G713- or 13q31-q33*-related biallelic marker in a control population according to the method of claim 35; and
c) determining whether a statistically significant association exists between said genotype and said trait.

37. A method of estimating the frequency of a haplotype for a set of biallelic markers in a population, comprising:
a) genotyping at least one *G713- or 13q31-q33*-related biallelic marker according to claim 29 for each individual in said population;
b) genotyping a second biallelic marker by determining the identity of the nucleotides at said second biallelic marker for both copies of said second biallelic marker present in the genome of each individual in said population; and
c) applying a haplotype determination method to the identities of the nucleotides determined in steps a) and b) to obtain an estimate of said frequency.

38. A method according to claim 37, wherein said haplotype determination method is selected from the group consisting of asymmetric PCR amplification, double PCR amplification of specific alleles, the Clark algorithm, or an expectation-maximization algorithm.

39. A method of detecting an association between a haplotype and a trait, comprising the steps of:
a) estimating the frequency of at least one haplotype in a trait positive population according to the method of claim 37;
b) estimating the frequency of said haplotype in a control population according to the method of claim 37; and
c) determining whether a statistically significant association exists between said haplotype and said trait.

40. A method according to claim 36, wherein said genotyping steps a) and b) are performed on a single pooled biological sample derived from each of said populations.

41. A method according to claim 36, wherein said genotyping steps a) and b) performed separately on biological samples derived from each individual in said populations.

42. A method according to either claim 36 or 39, wherein said trait is schizophrenia.

43. A method according to either claim 36 or 39, wherein said control population is a trait negative population.

44. A method according to either claim 36 or 39, wherein said case control population is a random population.

45. An isolated, purified, or recombinant polypeptide comprising a contiguous span of at least 6 amino acids of SEQ ID Nos 5 or 7.

46. An isolated or purified antibody composition are capable of selectively binding to an epitope-containing fragment of a polypeptide according to claim 45, wherein said epitope comprises:

- at least one of the amino acid positions 62 to 102 or 203 to 458 of SEQ ID No 5, and/or;
- amino acid positions 1 to 467 of SEQ ID No 7.

47. A method of determining whether an individual is at risk of developing schizophrenia, comprising:

a) genotyping at least one *13q31-q33*-related biallelic marker according to the method of claim 30; and

b) correlating the result of step a) with a risk of developing schizophrenia.

48. A method according to any one of claims 28, 35, 36, 37, 39 and 47 wherein said *13q31-q33*-related biallelic marker is selected from the group consisting of A12 to A49 and the complements thereof.

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49. A method according to claim 47, wherein said *13q31-q33*-related biallelic marker is selected from the following list of biallelic markers: A16 to A20, and the complements thereof.

50. A diagnostic kit comprising a polynucleotide according to any one of claims 3, 8, 12, 13 and 14.

51. A computer readable medium having stored thereon a sequence selected from the group consisting of a nucleic acid code comprising one of the following:

a) a contiguous span of at least 12 nucleotides of SEQ ID Nos 1, 2 or 3, or the complements thereof, wherein said contiguous span comprises at least one of the following nucleotide positions:

1 to 3236, 3547 to 3585 and 4649 to 5222 of SEQ ID No 1, or a variant thereof or a sequence complementary thereto;

1 to 16155 and 16331 to 21278 of SEQ ID No 2 or a variant thereof or a sequence complementary thereto; and

1 to 5531, 6844 to 7237, 7798 to 8184, 8667 to 9074, and 9356 to 21636 of SEQ ID No 3, or a variant thereof or a sequence complementary thereto;

b) a contiguous span of at least 12 nucleotides of SEQ ID No 31 or the complements thereof, wherein said contiguous span comprises at least one of the following nucleotide positions: 1 to 480 and 717 to 983 of SEQ ID No 31;

c) a contiguous span of at least 12 nucleotides of SEQ ID No 4 or the complements thereof, wherein said contiguous span comprises at least one of the following nucleotide positions: 1 to 519 and 2563 to 5566 of SEQ ID No 4;

d) a contiguous span of at least 12 nucleotides of SEQ ID No 6 or the complements thereof;

e) a contiguous span of at least 12 nucleotides of at least one of SEQ ID Nos 32 to 69, or the complements thereof; and

f) a nucleotide sequence complementary to any one of the preceding nucleotide sequences.

52. A computer readable medium having stored thereon a sequence consisting of a polypeptide code comprising a contiguous span of at least 6 amino acids of SEQ ID Nos 5 or 7.

53. A computer system comprising a processor and a data storage device wherein said data storage device a computer readable medium according to with claim 51 or 52.

54. A computer system according to claim 53, further comprising a sequence comparer and a data storage device having reference sequences stored thereon.

55. A computer system of Claim 54 wherein said sequence comparer comprises a computer program which indicates polymorphisms.

56. A computer system of Claim 53 further comprising an identifier which identifies features in said sequence.

57. A method for comparing a first sequence to a reference sequence, comprising the steps of:

reading said first sequence and said reference sequence through use of a computer program which compares sequences; and

determining differences between said first sequence and said reference sequence with said computer program,

wherein said first sequence is selected from the group consisting of a nucleic acid code comprising one of the following:

a) a contiguous span of at least 12 nucleotides of SEQ ID Nos 1, 2 or 3, or the complements thereof, wherein said contiguous span comprises at least one of the following nucleotide positions:

1 to 3236, 3547 to 3585 and 4649 to 5222 of SEQ ID No 1, or a variant thereof or a sequence complementary thereto;

1 to 16155 and 16331 to 21278 of SEQ ID No 2 or a variant thereof or a sequence complementary thereto; and

1 to 5531, 6844 to 7237, 7798 to 8184, 8667 to 9074, and 9356 to 21636 of SEQ ID No 3, or a variant thereof or a sequence complementary thereto;

b) a contiguous span of at least 12 nucleotides of SEQ ID No 31 or the complements thereof, wherein said contiguous span comprises at least one of the following nucleotide positions: 1 to 480 and 717 to 983 of SEQ ID No 31;

c) a contiguous span of at least 12 nucleotides of SEQ ID No 4 or the complements thereof, wherein said contiguous span comprises at least one of the following nucleotide positions: 1 to 519 and 2563 to 5566 of SEQ ID No 4;

d) a contiguous span of at least 12 nucleotides of SEQ ID No 6 or the complements thereof;

e) a contiguous span of at least 12 nucleotides of at least one of SEQ ID Nos 32 to 69, or the complements thereof;

f) a nucleotide sequence complementary to any one of the preceding nucleotide sequences; and

a polypeptide code comprising a contiguous span of at least 6 amino acids of SEQ ID Nos 5 or 7.